

What Approaches are Needed to Advance Proteomic Analysis?

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Loosely integrated perspective from:

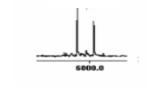
- Fallen population geneticist/biostatistician
- Interloping laboratory scientist
- Non-credentialed bioinformatician

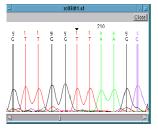


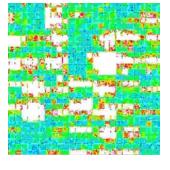


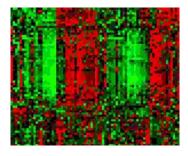
Scarred veteran of the molecular technology revolution ...

- Genetics
 - Southern blots
 - RFLPs
 - VNTRs
 - PCR-based
 - STRPs
 - Oligo-based assays
 - Mass spec.
 - Mapping
 - Linkage
 - association
- Genomics
 - Sequencing
 - Silver stained gels
 - Four color sequencing gel-based
 - Four color sequencing capillary
 - Transcript profiling
 - SAGE
 - cDNA array
 - Oligo nucleotide











- Initial promise always overstated
 - Innovator's dramatic finding required to break through
 - Insufficient experience with platform
 - known versus unknown demons
 - Disconnect with independent biologic/mechanistic validation



- Open is good!
 - Data sharing
 - Open source code
 - Analytic jamborees





- Standards versus standardization
 - Quality control
 - Experimental protocols
 - Standard external reference
 - Internal controls
 - Standard methodology
 - Data standards
 - Use established standards where they exist
 - Modify/extend existing standards where ever possible
 - Develop new standards "just in time"
 - Standards can NOT be proprietary





caCORE – common ontologic representation environment

- Information integration
- Cross-discipline reasoning

biomedical objects

common data elements





Enterprise Vocabulary

NCI Meta-Thesaurus

(Cross-map standard vocabularies/ontologies, e.g. SNOMED, MEDRA, ICD)

- Semantic integration, inter-vocabulary mapping
- UMLS Metathesaurus extended with cancer-oriented vocabularies
 - 800,000 Concepts, 2,000,000 terms and phrases
 - Mappings among over 50 vocabularies

NCI Thesaurus

- Description logic-based
- 18,000 "Concepts"
 - Concept is the semantic unit
 - One or more terms describe a Concept

 synonymy
 - Semantic relationships between Concepts

biomedical objects

common data elements





Common Data Elements

- Structured data reporting elements (e.g. LOINC)
- ISO11179 compliant

biomedical objects

common data elements





- Quality measures are transforming
 - Qualitative and quantitative
 - Objective measures critical





- The devil is in the details
 - Experimental inputs can be as critical as important as outputs
 - Laboratory information management systems (LIMS)





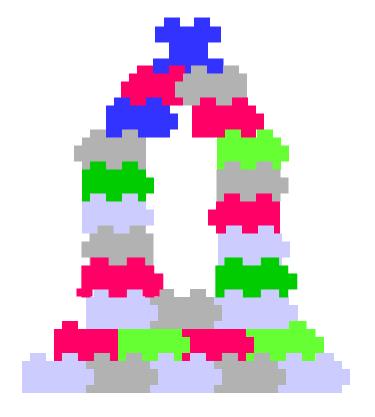
- Today's tools are not likely to be tomorrow's
 - Killer app's
 - Accessible, useful, user friendly apps critical to adoption
 - Not always the best approach (Eisen's cluster analysis)
 - Everything old is new again
 - On the shoulder's of giants...
 - Simpler methods are better
 - Design infrastructure that facilitates rapid exploration of new methods
 - Open source
 - Isolate data from applications
 - Component architecture





Components: software parts

- Small parts are better for building flexible shapes
- Have a uniform interface medium
- Snap-together connectivity
- Internals can be made from widely varying technologies



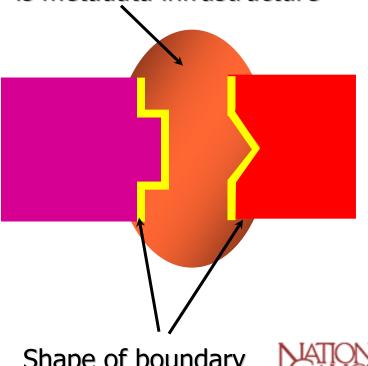




Boundaries and Interfaces

- focus on boundaries, interfaces, how things fit together,
- not on the internal details of how they're built: assume that will be diverse & changing

The glue that binds parts together is metadata infrastructure



Shape of boundary is defined in APIs





Biomedical Information Objects

- Computer model of a biomedical object – "Plato's Forms"
 - capture properties of object
 - can be joined together to make complex systems
 - isolate data from data source
 - isolate applications from data
- Examples:
 - HL7-RTM
 - MAGE-OM



common data elements



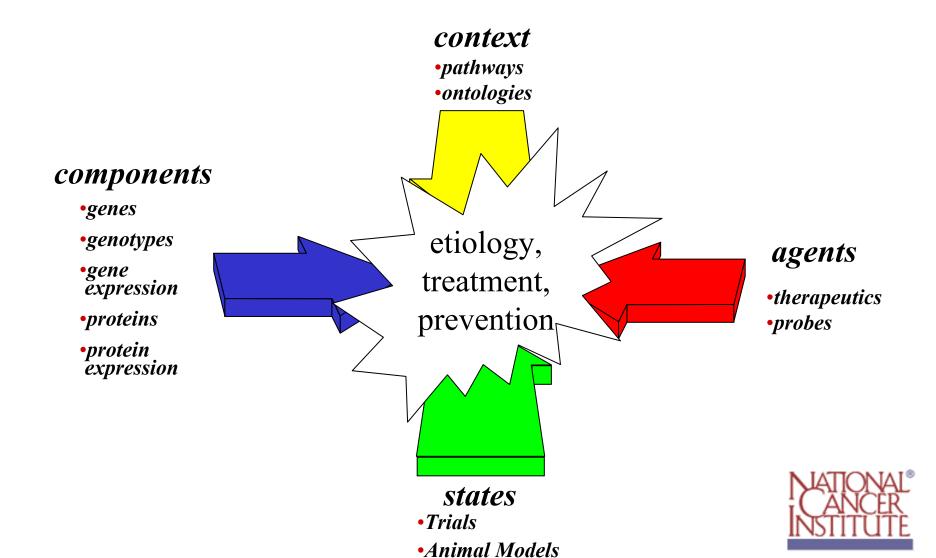
- Study design really does matter
 - New technologies ALWAYS initially appear to reduce the need for rigor
 - Animal models
 - Critical to validation
 - Clinical research considerations
 - Training/testing sets
 - validation sets
 - Over fitting





- You really are going to want to connect these results to other outcomes!
 - Other data types
 - Clinical outcomes





Pathway Database

- Enhance value of imperfect, but available, pathway knowledge
- Make biological assumptions explicit
- Merge data from separate pathways
- Build a causal framework to support (future) quantitative simulation/analysis



